

REPLACEMENT SHEET

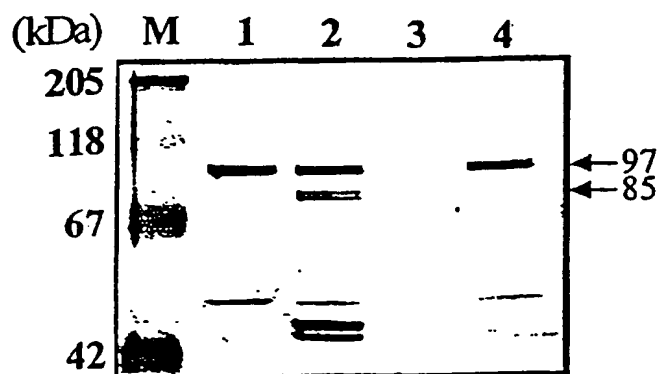
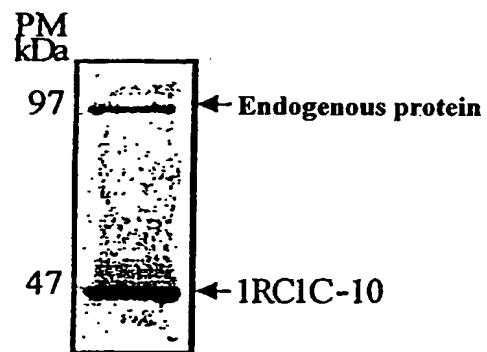


FIG.1

**REPLACEMENT SHEET**



**FIG. 2**

**REPLACEMENT SHEET**

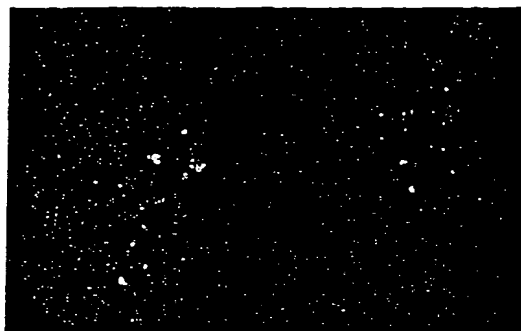


FIG. 3

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FIG. 4

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Fig. 5a

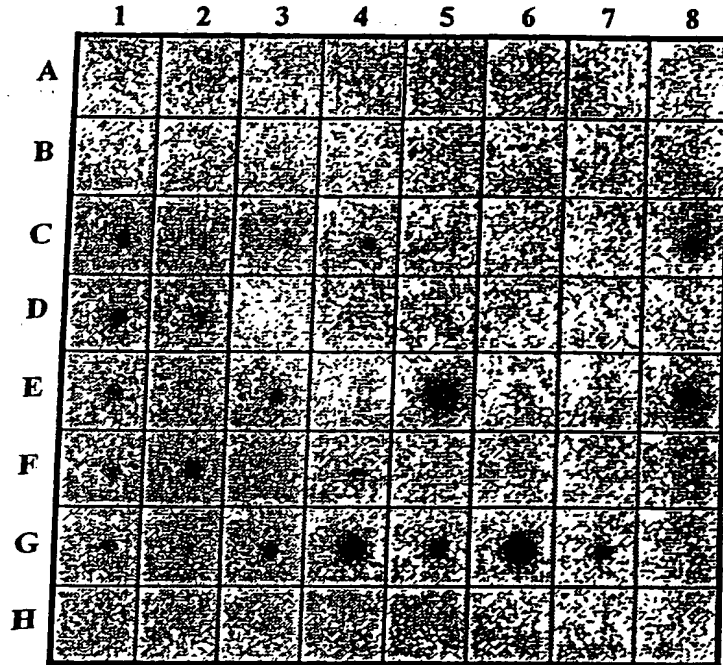


Fig. 5b

	1	2	3	4	5	6	7	8
A	whole brain	amygdala	caudate nucleus	cerebellum	cerebral cortex	frontal lobe	hippocampus	medulla oblongata
B	occipital lobe	putamen	substantia nigra	temporal lobe	thalamus	sub-thalamic nucleus	spinal cord	
C	heart	nervs	skeletal muscle	colon	bladder	uterus	prostate	stomach
D	testis	ovary	pancreas	pituitary gland	adrenal gland	thyroid gland	salivary gland	mammary gland
E	kidney	liver	small intestine	spleen	thymus	peripheral leukocyte	lymph node	bone marrow
F	appendix	lung	trachea	placenta				
G	fetal brain	fetal heart	fetal kidney	fetal liver	fetal spleen	fetal thymus	fetal lung	
H	yeast total RNA 100 ng	yeast tRNA 100 ng	E. coli rRNA 100 ng	E. coli DNA 100 ng	Poly r(A) 100 ng	human Cot1 DNA 100 ng	human DNA 100 ng	human DNA 500 ng

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1 ATGTGGATCC AGTTCGGAC CATGGATGG AGCAGACCC ACACGGTGA CTCGTGTCC AGCTGACCA AGGTGGAGGA 80  
81 GCTCAGGCGG AAGATCCAGG AGCTGTCCA CGTGGAGCCA GGCTGCAGA GGCTTTCTA CAGGGCAAA CAGATGGAGG 160  
161 ACGGCATAC CCTCTTCGAC TACGAGGTCC GCCTGAATGA CACATCCAG CTCCTGGTCC GCCAGACCT COTGCTCCCC 240  
241 CACACACCA AGGAGGGGA CTCCTGAGCTC TCCGACACG ATCCGGCTG CTGCTGGCC CAGATGAGT CAGACAAGTC 320  
321 TCTCACCCAC GGTGAGCGGG CCGCCGAGAC TGACACACGG CCAGCCCATG AGGACATGTG GAGTGAAGC GAATTGGGGC 400  
401 CTTCAAGGCT CAATGAGTAC GTGATGCTC GGACACAGAA CATGGGGCGG TGGTTTGAGG CGCAGGTGGT CAGGGTGACG 480  
481 CGGAAGCCC CCTCCCGGA CGAGCCCTGC AGTCCACGT CCAGGCCGGC GCTGGAGGAG GACGTCAATT ACCAGTGAA 560  
561 ATACGACGAC TACCCGGAGA ACGGGTGGT CCAGATGAAC TCCAGGGAGG TCCGAGCGG CCGCCGACC ATCATCAAGT 640  
641 GGCAGACCT GGAGGTGGC CAGGTGGTCA TGCTCAACTA CAACCCGAC AACCCCAAG AGCGGGGCTT CTGTACGAC 720  
721 GCGGAGATCT CCAGGAGCG CGAGACGAG ACGGCGCGG AACCTACGC CAACGTGGT CTGGGGGATG ATTCTTGAA 800  
801 CGACTGTCCG ATCATCTTCG TGGACGAAGT CTTCAAGATT GAGCGCGG GTGAAGGAG CCCCATGGT GACAACCCCA 880  
881 TGAGACGGAA GACGGGCGG TCTGCAAGC ACTGCAAGGA CGACGTGAAC AGACTCTGCA GGTCTGCGC CTGCCACCTG 960  
961 TCGGGGGCC GGCAGGACC CGACAAGCAG CTCATGTGG ATGAGTGGA CATGGCTTC CACATCTACT GCCTGGACCC 1040  
1041 GCCCTCAGC AGTGTTCGA CGGAGGACGA GTGGTACTGC CCTGAGTCC GGAATGATC CAGCGAGGTG GTACTGGCGG 1120  
1121 GAGAGCGCT GAGAGAGAGC AAGAGAATG CGAAGATGCG CTCGGGCACA TCGTCTCTAC AGCGGGACTG GGGCAAGGGC 1200  
1201 ATGGCCTGTG TGGCGCGCAC CAAGGAATGT ACCATCGTCC CGTCCAACA CTACGGACCC ATCCCGGGGA TCCCGTGGG 1280  
1281 CACCATGTGG CGGTTCCGAG TCCAGGTGAG CGAGTCGGT GTCCATCGC CCCACGTGCG TGSCATCCAT GGCCGGAGCA 1360  
1361 ACGAOGGATC GTACTOCCTA GTCTTGCGG GGGGCTATGA GGATGATGT GACCATGGA ATTTTTCAC ATACAGGGT 1440  
1441 AGTGTGTGTC GAGATCTTC CGGCACAAG AGGACCGGG AACAGTCTG TGATCAGAAA CTCACCAACA CCAACAGGGC 1520  
1521 GCTGGCTCTC AACTGCTTG CTCCCATCA TGACCAAGAA GGGGCGAGG CCAAGGACTG GCGTGGGGG AAGCGGTCA 1600  
1601 GGGTGTGTCG CAATGTCAAG GGTGGCAAGA ATAGCAAGTA CGCCCCCGT GAGGGCAACC GTACGATGG CATCTACAAG 1680  
1681 GTTGTGAAT ACTGGCCCGA GAAGGGGAAG TCCGGGTTTC TCGTGTGCG CTACCTTCTG CGGAGGGAGC ATGATGAGCC 1760  
1761 TGGCCCTTGG ACGAAGGAG GGAAGGACCG GATCAAGAG CTGGGGCTGA CCATGCAGTA TCCAGAAAGG TACCTGGAAG 1840  
1841 CCTGGCCAA CCGAGAGCGA GAGAGGAGA ACAGCAAGAG GAGGAGGAG GAGCAGCAG AGGGGGGCTT CGCGTCCCC 1920  
1921 AGGACGGCA AGGCAAGTG GAAGCGAAG TCGGCAGAG GTGGCCCGAG CAGGGCCGGG TCCCGCGCC GGCATCCAA 2000  
2001 GAAACCAAG GTGAGCCCT ACAGTCTAC GCGCCAGCAG AGCAGCTCA TCAGAGAGA CAGAGCAAC GCCAGCTGT 2080  
2081 GGAATGAGT CCTGCGTCA CTCAGGACC GCGCCGCGAG CCGCAGCCCG TTCCAGTTGT TCTGAGTAA AGTGGAGGAG 2160  
2161 AGCTTCCAGT GTATCTGCTG TCAGAGCTG GTGTTCCGGC CCATCACAC CTTGTGCCAG CACACGTGT GCAAGGACTG 2240  
2241 CTTGGACAGA TCTTTCGGG CACAGGTGT CAGTCCCTT GCTGCGCGT ACGACCTGG CCGCAGCTAT GCCATGCAAG 2320  
2321 TGAACAGOC TCTGCAGACC GTCTCTAACC AGCTCTTCCC CGGCTACGCG ATGGCCGGT GA 2382

FIG-6

REPLACEMENT SHEET

1	HWIQVTHDG	10	20	30	40	50	60	70	80
	RQHTVDSLS	RTKVEELR	KIQELFHVEP	GLQRLFYRGK	QHEDGHTLFD	YEVRLNDTIQ	LLVRQSLVLP		80
81	HSTKERDSEL	SQTDSCCLG	QSESDXSSTH	GEAAETDSR	PADEDMWDET	ELGLYKUNEY	VDARDTNMGA	WFEAQVVRVT	160
161	RKAPSRDEPC	SSTSRPALEE	DVIYHVKYDD	YPENGWVQMN	SROVRARART	IIKWQDLEVG	QVWHLNPNPD	NPKERGFWYD	240
241	AEISRKRETR	TARELYANVV	LGDDSLNDCR	IIFVDEVFKI	ERPGEGSPMV	DNPHRRKSOP	SCHCKRDDVN	RLCKVCACHL	320
321	CGGRQDPDKQ	LMCDECDMAF	HIYCLDPPLS	SVPSEDEWYC	PECRNDASEV	VLAGERLRES	KKNAKMASAT	SSSQRDWGRG	400
401	MACVGRTEKC	TIVPSNHYGP	IPGIPVGTMW	RFRVQVSESG	VHRPHVAGIH	GRSNDGSYSL	VLAGGYEDDV	DHGNFFTYTG	480
481	SGGRDLSGNK	RTAEQSCDQK	LTNTNRALAL	NCFAPINDQE	GAEAKDWRSG	KPVRVVRNVK	GGKNSKYAPA	EGNRYDGIYK	560
561	VVKYMPKGR	SGFLVMRYLL	RRODDEPGPW	TREGKDRIKK	LGLTMQYPEG	YLEALANRR	EKENSKREEE	EQEGGFASP	640
641	ATGKGWKRK	SAGGQPSRAG	SPRRTSKTKK	VEPYSLTAQQ	SSLIREDKSN	AKLMNEVLAS	LADRPASGSP	FQLFLSKVEE	720
721	TFQCICQEL	VTRPITTVCQ	HNVCRCCLDR	SFRAQVFSCP	ACRYDLORSY	AMQVNPQLQT	VLNQLFPGYG	NGR*	794

FIG-7

REPLACEMENT SHEET

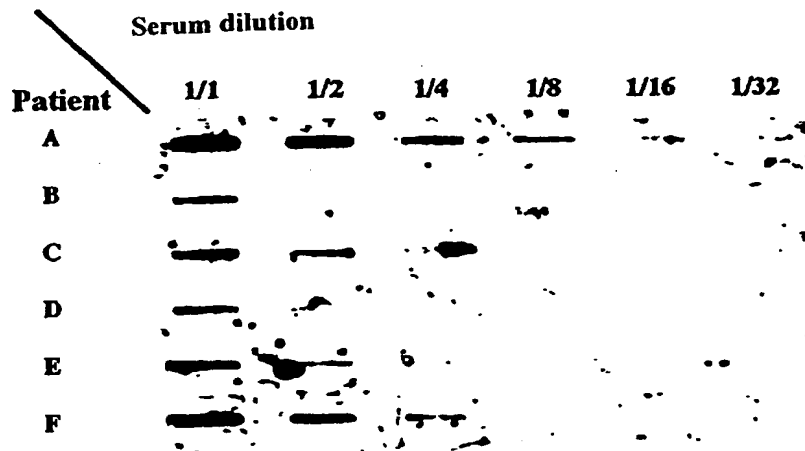
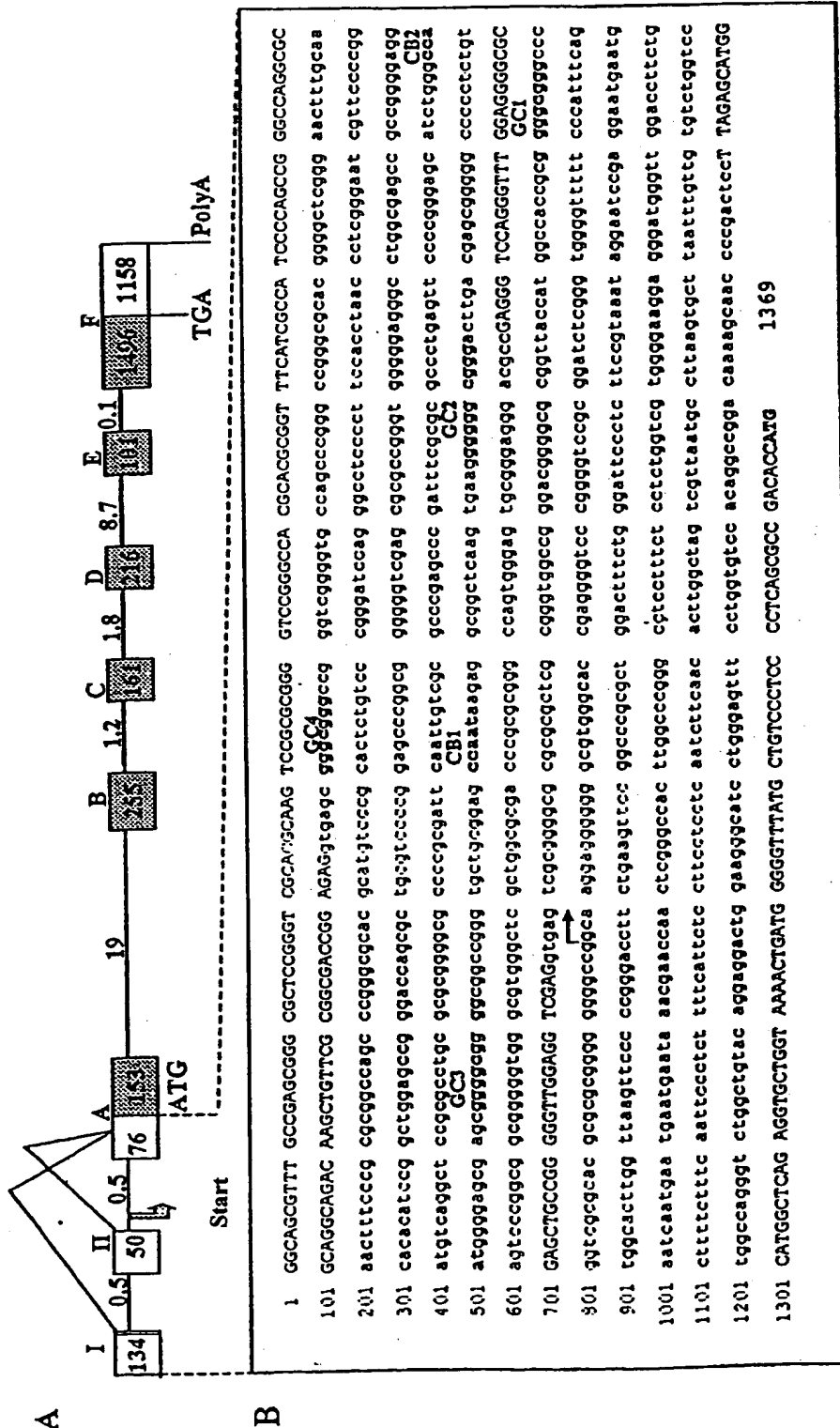


FIG-8



REPLACEMENT SHEET

FIG-9



REPLACEMENT SHEET

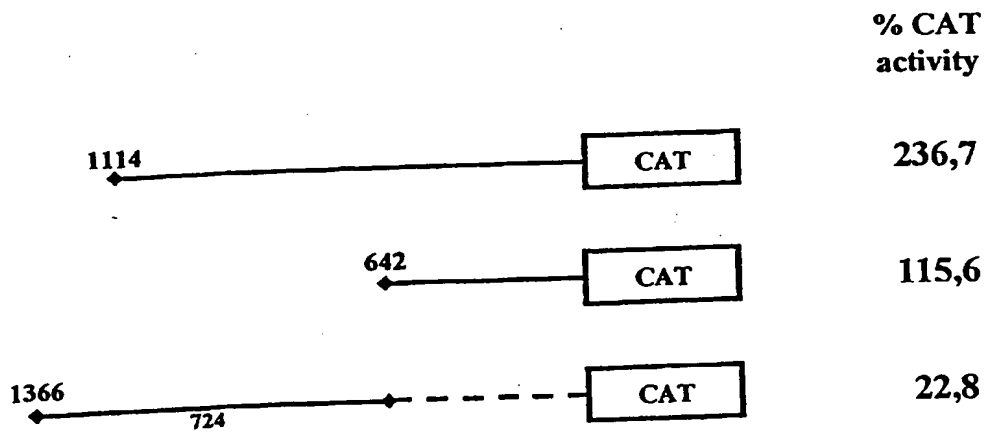


FIG 10

REPLACEMENT SHEET

FIG-11A

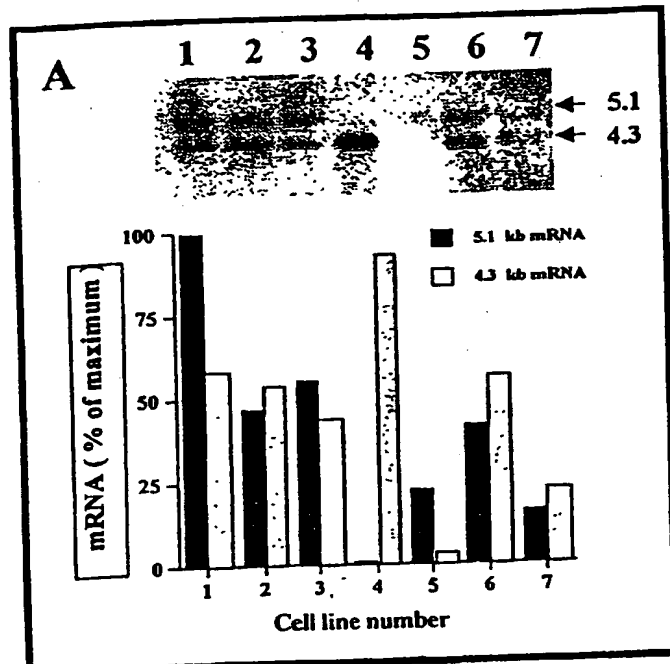


FIG-11B

